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Research article

INFLUENCE OF DIRECT AND MATERNAL EFFECTS ON CARCASS LENGTH AS A SECONDARY TRAIT IN CARCASS EVALUATION IN INDIGENOUS MATEBELE GOATS OF ZIMBABWE.

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ABSTRACT: Genetic parameter estimation for simple carcass traits has been confined to the improved goat breeds worldwide unlike in the unimproved breeds in developing countries where goats are numerous. Variance components for additive direct, additive maternal, permanent environmental maternal effects, the covariance between additive direct and maternal effects were estimated by restricted maximum likelihood, fitting five animal models from 2341 (1359 males; 982 females) carcass length pedigree records collected over a period of 13 years (1984- 1997) of indigenous Matebele goat of Zimbabwe. All investigated models included a random direct genetic effect, but different combinations of random maternal genetic and permanent environmental maternal effects as well as direct-maternal genetic covariance. The analytical models included fixed effects of sex, age at slaughter and year of slaughter. The direct heritability (h^2_a) ranged from 0.49 to 0.12 when the maternal genetic effects were included in the model, whereas h^2_a estimate was 0.32 when maternal effects were excluded. The maternal heritability (h^2_m) was 0.00 when only maternal genetic effect was included in the model and were 0.12 and 0.02 when the permanent environmental effect of the dam was added. The permanent environmental effect of the dam was negligible. A weak negative covariances between direct and maternal genetic effects (σ^2_{am}) was observed when maternal genetic effects and permanent environmental maternal effects were accounted for in the model. A animal model with both direct additive maternal genetic effects and permanent environment effects as the random effects other than the residuals was the best model for genetic evaluation of carcass length in indigenous Matebele goat.
Key words*:* Variance Components, Animal Model, Carcass length, Indigenous Matebele Goat

INTRODUCTION

Africa's goat population increased by 75% between 1980 and 2005 and constitutes 30% of the world population. [15]. In the country, goat population is 4.4 million and rising [2] of which 90% of the national flock is owned by smallholder farmers [7]. Globally, the number of goats has also increased even in countries with high and medium income [12].

Estimates of genetic parameters for carcass length as a useful secondary trait using different animal models in the tropics for indigenous goats are scarce in literature. Models with maternal effects and corresponding genetic parameters have always been considered problematic [10] due to the confounding contributions of direct and maternal effects.

The animal models commonly used to estimate maternal effects include maternal genetic and permanent environmental effects [19]. Genetic models, including maternal effects and the covariance of direct and maternal genetic effects, fit data better than the simple additive model [10]. The aim of this study was to investigate the importance of direct and maternal effects on hot carcass weight of the indigenous Matebele goat, using different animal models.

MATERIALS AND METHODS

Location

Matopos Research Station (20 ^{0} 23$^{'}$ S, 31^{0} 30$^{'}$ E) situated 30 km South West of Bulawayo in Zimbabwe on an altitude of 800m above sea level which experiences low erratic rainfall of less than 450mm per annum [7]. High summer temperatures, maximum and minimum mean temperatures of hottest months are 31.6 ^{0} C and 21.4 ^{0} C, respectively with a possibility of severe droughts [6]. The most common type of vegetation is sweet veld with comparatively high nutritional value of browse and annual grass species [17]. Detailed description of the climate and vegetation type were given by [3] and [4] respectively.

Flock management

The does plus their progeny were grazed on an extensively managed dry land veld during the day from 0800 hours to 1500 hours and were penned at night. The major grass species in these pastures are *Hyparrhenia* spp., *Andropogon* spp., *Pennisetum purpur* and *Brachiaria mutica*. Depending on the availability of food and the severity of dry season, varying quantities of energy (maize stover) and protein (cotton seed cake) supplements were given when does grazed on standing hay or cut and stacked hay. The does were fed 0.3 kg and kids 0.2 kg of cottonseed cake meal each per day from the end of May each year until the onset of the rainy season. The nutrient composition of cotton seed cake was 930g/kg dry matter, 730g/kg total digestible nutrient, 390-450g/kg protein, 300-360g/kg digestible protein and metabolizable Energy value 10.9 megajoules/kg. Water was constantly available. Mineral licks were often *ad libitum* in the dry season. Prophylaxis deworming and de-ticking in a plunge dip were regularly carried out using organophosphates. All animals were vaccinated against Pulpy Kidney and Rift Valley Fever. Does were assigned into mating flocks each year but mating of close relatives was avoided. Does of all age categories were represented in each single buck-mating group. The breeding season was between May and June. Single sire flocks comprised of one buck to 30 does. Females were introduced to the breeding flock for mating when they attained one and half years of age and bucks were not used for service until they were over one and half years. Initial buck selection was based on birth weights with male singles of over 3 kg and twins over 2.5 kg weight being retained entire, while the rest of the males were castrated using rubber ring. Most kids were born between late October and early November, which is the start of the rainy season. Kids were weighed using an electronic scale and ear tagged soon after birth and left to suckle their dams during grazing until weaning at approximately 3 months of age. Kids were separated by sex at weaning into different weaner flocks.

Slaughter Method

Goats of an average age of 21 months raised on range were slaughtered without being fattened. They were not given any feed for 24 hours before slaughter but only provided with fresh drinking water. The animals were weighed individually before fasting (preslaughter weight) and 24-hour fasting (empty live weight just before slaughter. Heart girth was also measured at the time of slaughter. Slaughtering was performed according to the local method of severing jugular veins, throat and trachea without stunning. The slaughtered animals were allowed to bleed to their end usually for 10 minutes and the head was then removed at its atlanto-occipital articulation followed by flaying, evisceration and disjoining of cannons. The weight of the head, feet and skins were recorded separately. The entire gastro-intestinal tract was removed from each slaughtered goat and weighed with and without contents. A hot carcass of each animal was prepared by removing head, feet, skin, thoracic cavity contents, abdominal cavity contents, pleural cavity contents and cannons. This was weighed within one hour of slaughter.

Liver, lungs, heart, kidneys, kidney fat were removed from the body cavity and weighed separately. The dressed carcasses were chilled at –20^{c} for 24 hours which led to shrinkage in carcass. Cold carcass was obtained before cutting the carcass into different prime cuts. The weight of prime cuts (front barrel and hind barrel) was also recorded. The last rib was left attached to the hind barrel. The chilled carcass was split between the 6th and 7th ribs to obtain the rib barrel. Fat score on back fat was done by visual assessment using a scale of 1 to 3.5 designed by International Livestock Centre for Africa.

Statistical methods

Data on carcass length were obtained from Matopos Research Station, Bulawayo, Zimbabwe on indigenous Matebele goat. The data included a total of 2341(1359 males and 982 females) pedigree carcass length records from 87 sires and 218 dams of the indigenous Matebele goat. Genetic parameters were estimated using the Average Information Restricted Maximum Likelihood (AIREML) methodology [5] using an Animal Model. The analytical models included fixed effects of sex, age at slaughter and year of slaughter. Fixed factors for models for all traits were determined through preliminary analyses using procedure GLM of SAS (1996) (SAS Inst. Inc., Cary, NC). Fixed factors (main effects and interactions) and covariates were tested and removed from the model if found non-significant (P> 0.01), with non-significant effects rejected sequentially. A simplex algorithm is used to search for variance components to minimize the function, -2log likelihood (L). Convergence was assumed when the variance of the fuction values (-2logL) of the simplex was $<10^{-8}$. A log likelihood ratio test was used to choose the most suitable random effects model for post weaning growth. The reduction in -2 log L when a random effect was added to the model was calculated. If this reduction was greater than the value of the Chi-square distribution with one degree of freedom ($p<0.05$) the additional random effect fitted was considered significant. When log likelihood did not differ significantly ($p>0.05$), the model that had the fewer number of parameters was selected as the most appropriate. Five different animal models were fitted for carcass length by ignoring or including maternal genetic effect, covariance between direct-maternal effects, maternal environmental effect that the five different models were:

Model 1 was a model with animal additive genetic effects and maternal genetic effect as the random effect other than the residuals:

$y=Xb + Z_a a + Z_m m + e$ (1)

Model 2 included random effect of permanent maternal environment

$y=Xb + Z_a a + Z_c c + e$ (2)

Model 3 included both permanent environmental and genetic maternal effects but did not allowed correlation between direct and maternal genetic random effects.

$y=Xb + Z_a a + Z_m m + Z_c c + e$ $Cov(a,m)\neq A\sigma_a m$ (3)

Model 4 was the same as model 3 but assumed correlation between direct and maternal genetic random effects.

$y=Xb + Z_a a + Z_m m + Z_c c + e$ $Cov(a,m)= A\sigma_a m$ (4)

Model 5 excluded permanent environmental and maintained genetic maternal effects but allowed correlation between direct and maternal genetic random effects.

$y=Xb + Z_a a + Z_m m + e$ $Cov(a,m)=A\sigma_a m$ (5)

where Y is the vector of observations b, a, m, c and e are the vectors of fixed effects, direct additive genetic effects (animal), maternal genetic effects, permanent environmental effect of dam and the residual, respectively. X, Za, Zm, and Zc, are the incidence matrices of fixed effects, direct additive genetic effects, maternal genetic effects and permanent environmental effect of dam. (Co)variances were described as: $V(a) = \sigma^2_a A$, $V(m) = \sigma^2_m A$, $V(c) = \sigma^2_c I$, $V(e) = \sigma^2_e I$ and $Cov(a,m) = \sigma_{am} A$, where σ_{am} is the covariance between direct and maternal genetic effects, σ^2_a the direct additive genetic variance, σ^2_m the maternal genetic variance, σ^2_c the variance of the permanent environmental effect of the dam and σ^2_e the variance of the residuals. A is the numerator relationship matrix between animals, I the identity matrix. In the present study the fixed part of the model included age at slaughter, sex and year of slaughter of progeny. Heritability of total additive genetic contribution to a maternally influenced trait was calculated according to the following equation [20].

$$h^2_T = \frac{\sigma^2_a + 0.5\sigma^2_m + 1.5\sigma^2_{am}}{\sigma^2_p}$$

Appropriate model selection using Mallows C_p Statistic

Siniksaran (2008) suggested the Mallows' C_p statistic that is of the form, $C_p = \frac{RSS_p}{s^2 - (n-2p)}$ (1)

where RSSp is the residual sum of squares from an animal model containing p parameters, p is the number of parameters in the model including ß0, s2 is the residual mean square from the largest postulated containing all the effects and n is the total number of records. s2 is presumed to be a reliable unbiased estimate of the error of variance σ2, i.e.

$$E\left(s^2\right) = \sigma_e^2 \tag{2}$$

If we assume that an equation with p parameters does not suffer from lack of fit then

$$E\left(RSS_p\right) = \left(n - p\right)\sigma_e^2 \tag{3}$$

Substituting equations (2) and (3) into equation (1), the Mallows Cp statistic becomes

$$C_p = \frac{\left(n - p\right)\sigma_e^2}{\sigma_e^2 - \left(n - 2p\right)} \tag{4}$$

Taking the expectation of equation (4) gives $E\left(C_p\right) = p$, which follows that a plot of C_p versus p will show up the "adequate models" as points fairly close to the $C_p=p$ line. Points representing well-fitting models likewise are expected to fall below the $C_p=p$ line because of random variation.

RESULTS AND DISCUSSION

The descriptive statistics of the data set, covariance components and Cp statistic values under five different animal models regarding carcass length are shown table 1, 2 and 3, respectively. It is evident that the model used in the analysis influenced the relative values of direct heritability and maternal heritability. Estimates of the direct heritability had a range of 0.12 to 0.49 and estimates of the maternal heritability were low ranged from zero to 0.02. Maternal heritability were lower than direct heritability in all models which was an indication that carcass length was largely influenced by the individual genetic potential than the maternal genetic potential. In current study on carcass length of indigenous Matebele goat the inclusion of both maternal genetic and permanent environmental maternal effects, with covariance between direct and maternal effects gave the least Cp statistic value. In Model 3 in which both maternal genetic effects and the permanent environmental maternal effects were included permanent environmental maternal effects contribute only 1 % of the total phenotypic value. Excluding maternal genetic effects in Model 2 resulted in a decrease in direct heritability by 35% compared to Model 1 with direct genetic effects alone, which may assume that maternal genetic effect may be important for carcass length. In fact in Model 3 in which direct animal effects, maternal genetic effects and permanent environmental effects were taken into account without covariance between direct and maternal effects, 37% and 12% of the total phenotypic variance was attributable to direct animal effects and maternal genetic effects, respectively. When one of the maternal effects were ignored the total variance was more attributed to the direct genetic variance resulting in overestimating of direct heritability. Inclusion of a covariance between direct and maternal effects in Model 5 without taking into account permanent environmental effects resulted in lowest total genetic effects. The high total genetic effects in Model 4 was not drastically reduced as compared to Model 3 possibly because of the weak negative correlation (r_{AM}) of direct and maternal genetic effects. The nature of the correlations which may be positive or negative can in weight traits sometimes be attributed to structure of the data [9, 13]. In the present study Model 4 which included both permanent environmental and genetic maternal effects and allowed correlation between direct and maternal genetic random effects was found to be appropriate for genetic evaluation of carcass length in this population as indicated by the least Cp value (Table 3).

Table 1.Structure and descriptive statistics of the data set of hot carcass weight of Matebele goats of Zimbabwe

Item	Model
Pedigree records	2341
No base parents	255
No animals	2596
No sires	87
No dams	218
Mean (kg)	12.81
Coefficient of Determination (%)	57
Coefficient of Variation (%)	20.97
Standard Deviation (kg)	2.93

Table 2.Estimates of covariance components and genetic parameters of carcass length in indigenous Matebele goat of Zimbabwe.

Item	Model 1	Model 2	Model 3	Model 4	Model 5
σ^2_a	41.93	25.71	33.39	28.92	8.89
σ^2_m	0.46		10.52	1.38	0.19
σ^2_{am}				-0.20	-0.30
σ^2_{pe}		0.37	0.78	0.25	
σ^2_e	44.33	54.68	45.99	52.02	67.19
σ^2_p	86.72	80.76	90.68	82.37	75.97
h^2_a	0.49	0.32	0.37	0.35	0.12
h^2_m	0.00		0.12	0.02	0.00
r_{am}				-0.03	-1.00
c^2		0.01	0.01	0.00	
h^2_T	0.49	0.32	0.49	0.37	0.12

σ^2_a = direct additive genetic
σ^2_m = maternal additive genetic variance
σ^2_{am} = direct and additive variance
σ^2_{pe} = permanent environmental dam variance
σ^2_p = phenotypic variance = sum of variance and covariance components
σ^2_e = error variance
h^2_a = direct heritability
h^2_m = maternal heritability
h^2_T = total heritability (total genetic effect)
r_{am} = direct and maternal genetic correlation

Table 3. The computed Mallows C_P statistic used to rank animal models for carcass length in indigenous Matebele goat

Model	CP	Ranking
4	10.23	1
2	11.06	2
1	11.55	3
3	11.75	4
5	12.03	5

CONCLUSION

The study shows that inclusion of maternal genetic and/or permanent environmental effects in animal models for carcass length of indigenous Matebele as a secondary trait will influence the magnitude of direct heritability. Maternal heritability were lower than direct heritability estimates, indicating a greater genetic influence of individual animal's genetic potential than the influence of maternal effects on carcass length. In general due to the contribution of maternal effects to phenotypic variance analyzed trait, maternal genetic and maternal environmental effects should be taken into account in genetic evaluation for carcass length if needs arise.

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